130588.00025.ST25.txt SEQUENCE LISTING

, 1

Gln Tyr

```
Arizona Board of Regents, acting for and on behalf of,
<110>
       Arizona State University (ABR/ASU)
       Massia, Stephen P.
       Ehteshami, Gholam R.
       Bioselective bioconjugates for
<120>
       anti-inflammatory/immunosuppressant therapies
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       10/295,734
       2002-11-15
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130588.00025.ST25.txt

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	Inr	ьeu	Pne	_	TÀT	ser	irp	цец		ser	UIS	GLY	AIA		Arg	Trp ·	
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•			H H			~~~	***	~~	+		~~~		~~~		~~~	~~+	2
	cag 40		_	_									gag				2
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Thr	Leu	Phe	Gly 20	Tyr	Ser	Trp	Leu	His 25	Ser	His	Gly	Ala	His 30	Arg	Trp
Leu	Leu	Val 35	Gly	Ala	Pro	Thr	Ala 40	Met	Trp	Leu	Ala	Met 45	Ala	Ser	Val
Ile	Asn 50	Pro	Gly	Ala	Ile	Tyr 55	Arg	Cys	Arg	Ile	Gly 60	Lys	Asn	Pro	Gly
Gln 65	Thr	Cys	Glu	Leu	Gln 70	Leu	Gly	Ser	Phe	His 75	Gly	Glu	Pro	Gly	Gly 80
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Ser	Arg														

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                                     10
                                                          15
1
ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
            20
                                 25
                                                      30
gga tot toa tac tgg aca gga ago tta ttt gta tac atg att acc act
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
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                                                  45
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Asn Lys Tyr Lys
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130588.00025.ST25.txt
Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
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Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
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Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
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                                     10
                                                          15
1
ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
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20 25 30

gga tct tca tac tgg aca gga agc tta ttt gta tac atg att acc act 44 Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr

Page 9

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45

35

10

Asn Lys Tyr Lys

50

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Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr 35 40 45

Asn Lys Tyr Lys 50

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                                     10
                                                          15
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aca ittg tit ggg tat agt tgg cit cat agt cat gga gca cac aga tgg
Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp
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                                 25
                                                      30
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Leu Leu Val Gly Ala
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2

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cag gtg aag cca gga agt tat tta ggg tat agt gta ggt gcc ggc cat 96

Gln Val Lys Pro Gly Ser Tyr Leu Gly Tyr Ser Val Gly Ala Gly His

20 25 30

ttc aga agt caa cac acg aca gaa gtt gtc ggc ggt gca cca caa cat 44

Phe Arg Ser Gln His Thr Thr Glu Val Val Gly Gly Ala Pro Gln His

35 40 45

gag cag ata gga aaa gct tac atc ttt agt ata gat gaa aaa gaa tta

1

2

92

Glu Gln Ile Gly Lys Ala Tyr Ile Phe Ser Ile Asp Glu Lys Glu Leu

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Phe Arg Ser Gln His Thr Thr Glu Val Val Gly Gly Ala Pro Gln His
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Glu Gln Ile Gly Lys Ala Tyr Ile Phe Ser Ile Asp Glu Lys Glu Leu
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1
                                     10
                                                          15
gat ggc ttc tca gac ctg ctc gtc ggt gct ccc atg caa tcg acg ata
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Arg	Glu	Glu	Gly	Arg	Val	Phe	Val	Tyr	Ile	Asn	Ser	Gly	Ser	Gly	Ala	
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65 999 88 Gly 99a 36	ttt Phe	gaa Glu atc	gac Asp	gta Val 85	70 gcg Ala	att Ile	gga Gly	gca Ala aga	cca Pro 90	75 cag Gln gat	gag Glu ggt	gac Asp	gat Asp	ctc Leu 95 tca Ser	80 cag Gln	
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80 Val	Asp	Val	Ala	Val	Gly	Ala	Phe	Arg	Ser	Asp	Arg	Ser	Asp	Ser	Ala		
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gtt 28	ttg	tta	aga	acg	cgt	cca	gtc	gtc	ata	gtg	gac	gct	tca	ctt	agt		5
	Leu	Leu	Arg	Thr	Arg	Pro	Val	Val	Ile	Val	Asp	Ala	Ser	Leu	Ser		
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24 Trp	Pro	Ser	Val	Cys	Ile	Asp	Leu	Thr	Leu	Cys	Phe	Ser	Tyr	Lys	Gly		
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72		gtt										•					6
Lys		Val	Pro	GIA	Tyr		Val	Leu	Pne	Tyr		Met	ser	Leu	Asp		
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225					230					235					240		

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	16												gac					8
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4	19									Ala								
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Val	Leu	Leu	Arg	Thr 165	Arg	Pro	Vál	Val	Ile 170	Val	Asp	Ala	Ser	Leu 175	Ser
His	Pro	Glu	Ser 180	Val	Asn	Arg	Thr	Lys 185	Phe	Asp	Cys	Val	Glu 190		Gly
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Gly Asn Leu Thr Tyr Gly Tyr Val Thr Ile Leu Asn Gly Ser Asp Ile
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Val Ala Asp Ser Ile Gly Phe Thr Val Glu Leu Gln Leu Asp Trp Gln 275 280 285

Lys Gln Lys Gly Gly Val Arg Arg Ala Leu Phe Leu Ala Ser Arg Gln 290 295 300

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Ser Gly Glu Gln Met Ala Ser Tyr Phe Gly Tyr Ala Val Ala Ala Thr 50 55 60

Asp Val Asn Gly Asp Gly Leu Asp Asp Leu Leu Val Gly Ala Pro Leu 65 70 75 80

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Tyr Val Tyr Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu 100 105 110

Thr Leu Thr Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr
115 120 125

Pro Leu Gly Asp Leu Asp Gln Asp Gly Tyr Asn Asp Val Ala Ile Gly
Page 31

135

140

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Gly	Gly	Pro	Gly	Gly 165	Leu	Gly	Ser	Lys	Pro 170	Ser	Gln	Val	Leu	Gln 175	Pro
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96	_						gat -		_		_				
Thr	Glu	Lys	Glu	Pro	Leu	Ser	Asp	Pro	Val	Gly	Thr	Cys	Tyr	Leu	Ser

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Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys Arg Ser Asp 35 40 45

Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly Phe Ser Ala 50 55 60

Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro Gly Ser Tyr 70 75 80

Phe Trp Gln Gly Gln Ile Leu Ser Ala Thr Gln Glu Gln Ile Ala Glu 85 90 95

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aaa

51 Lys

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aga
51
```

Arg

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                                                          15
gga agt ata atc cca cat gac ttt
72
Gly Ser Ile Ile Pro His Asp Phe
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20

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                                                         15
                5
                                     10
1
aaa agt aag aca tta ttc agt
Lys Ser Lys Thr Leu Phe Ser
```

20.

aga gaa

Arg Glu

54

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                5
                                     10
1
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                                     10
                                                          15
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Trp Arg
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1
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								٠	-							
act 96	tgg	tcg	tgg	aca	tta	ggc	gca	gtc	gag	ata	ctc	gac	agt	tat	tat	
	Trp	Ser	Trp	Thr	Leu	Gly	Ala	Val	Glu	Ile	Leu	Asp	Ser	Tyr	Tyr	
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		35					40					45				
	agc	gta	gcg	gta	acg	gat	gtg	aac	gġa	gac	ggc	cgc	cat	gac	ttg	1
92 His	Ser	Val	Ala	Val	Thr	Asp	Val	Asn	Gly	Asp	Gly	Arg	His	Asp	Leu	
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	gtt	gga	gct	ccg	ctc	tac	atg	gag	agt	cga	gca	gat	cgc	aag	ctț	2
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	gaa	gtg	ggc	cga	gta	tat	ctt	ttc	ctt	caa	сса	cgg	ggt	ccc	cac	2
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Page 54

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gcc 36	cta	ggc	gct	cct	agt	tta	ttg	tta	acc	gga	aca	cag	ttg	tat	ggţ	3
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80 Gly	Gln	Val	Leu	Val	Phe	Leu	Gly	Gln	Ser	Glu	Gly	Leu	Arg	Ser	Arg	
145					150			٠		155					160	
ccg 28	tct	caa	gtc	tta	gac	tcg	cca	ttt	cca	acc	gga	agt	gcg	ttt	<b>a</b> aa	5
	Ser	Gln	Val	Leu	Asp	Ser	Pro	Phe	Pro	Thr	Gly	Ser	Ala	Phe	Gly	
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ttc 76	agt	ctc	cgt	ggt	gca	gtg	gac	atc	gat	gac	aat	ggt	tac	ccg	gat	5
. •	Ser	Leu	Arg	Gly	Ala	Val	Asp	Ile	Asp	Asp	Asn	Gly	Tyr	Pro	Asp	
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cta 24	att	gtt	gga	gcc	tac	999	gcc	aat	caa	gta	gca	gtạ	tat	cgg	gcg	6
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								Page	55							

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Gln	Pro	Val	Val	Lys	Ala	Ser	Val	Gln	Leu	Leu	Leu	Gln	Asp	Ser	Leu		
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	_											-					
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Thr	Trp	Ser	Trp 20	Thr	Leu	Gly	Ala	Val 25	Glu	Ile	Leu	Asp	Ser 30	Tyr	Tyr		
Gln	Arg	Leu 35	His	Arg	Leu	Arg	Ala 40	Glu	Gln	Met	Ala	Ser 45	Tyr	Phe	Gly		
His	Ser 50	Val	Ala	Val	Thr	Asp 55	Val	Asn	Gly	Asp	Gly 60	Arg	His	Asp	Leu		
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Leu 65	Val	Gly	Ala	Pro	Leu 70	Tyr	Met	Glu	Ser	Arg 75	Ala	Asp	Arg	Lys	Leu 80		
Δla	Glu	Val	Glv	Ara	Val	Tvr	Len	Phe	Leu	Gln	Pro	Arg	G] v	Pro	His		
1114	CIU		1	5	-	-1-		Page				3	1				

85 · 90 95

Ala Leu Gly Ala Pro Ser Leu Leu Leu Thr Gly Thr Gln Leu Tyr Gly
100 105 110

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Arg Asp Gly 115 120 125

Tyr Asn Asp Ile Ala Val Ala Ala Pro Tyr Gly Gly Pro Ser Gly Arg 130 135 140

Gly Gln Val·Leu Val Phe Leu Gly Gln Ser Glu Gly Leu Arg Ser Arg 145 150 155 160

Pro Ser Gln Val Leu Asp Ser Pro Phe Pro Thr Gly Ser Ala Phe Gly 165 170 175

Phe Ser Leu Arg Gly Ala Val Asp Ile Asp Asp Asn Gly Tyr Pro Asp 180 185 190

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	Gly	Tyr	Tyr	Phe	Leu	Gly	Leu	Leu	Ala	Gln	Ala	Pro	Val	Ala	Asp	
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gtc 36	gag	ata	tta	gat	agc	tac	tac	caa	cgc	tta	cac	aga	ttg	cgt	gct	3
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Va:	l Glu	Ile	Leu	Asp	Ser			Gln				Arg	Leu	Arg	Ala	
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			100					103					110			
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84	ı Gln								•							
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ASI	n Gly	Asp	GIY	Arg	HIS		шeu	ьец	vai	GIA		PIO	пец	ıyı	Mec	
	130					135					140					
~ ~		200	~~~	~~~~		226	<b>++</b> ~	aat.	~ .	at a	~~~	202	at t	tst	tta	. 4
80	g agc								•					-		4
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149	5				150					155	•				160	
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	e Leu	Gln	Pro	Arg	Gly	Pro	His	Ala	Leu	Gly	Ala	Pro	Ser	Leu	Leu	
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Phe	Pro	Thr	Gly	Ser	Ala	Phe	Gly	Phe	Ser	Leu	Arg	Gly	Ala	Val	Asp	
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Ile	Asp	Asp	Asn	Gly	Tyr	Pro	Asp	Leu	Ile	Val	Gly	Ala	Tyr	Gly	Ala	
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Page 61

<223> Description of Artificial Sequence: Integrin

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Gln Ser Leu Ser Phe Asp Ser Ser Asn Pro Glu Tyr Phe Asp Gly Tyr 50 55 60

Trp Gly Tyr Ser Val Ala Val Gly Glu Phe Asp Gly Asp Leu Asn Thr 70 75 80

Thr Glu Tyr Val Val Gly Ala Pro Thr Trp Ser Trp Thr Leu Gly Ala 85 90 95

Val Glu Ile Leu Asp Ser Tyr Tyr Gln Arg Leu His Arg Leu Arg Ala 100 105 110

Glu Gln Met Ala Ser Tyr Phe Gly His Ser Val Ala Val Thr Asp Val 115 - 120 125

Asn Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro Leu Tyr Met 130 135 140

Glu Ser Arg Ala Asp Arg Lys Leu Ala Glu Val Gly Arg Val Tyr Leu 145 150 155 160

Phe Leu Gln Pro Arg Gly Pro His Ala Leu Gly Ala Pro Ser Leu Leu 165 170 175

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                                                     270
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tgc 96	gtc	tgc	ggc	caa	tgt	gta	tgc	cgg	aaa,	cgt	gac	aac	aca	aac	gaa	
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15

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	tta 92	atg	aac	gag	atg	aga	aga	atc	act	tca	gac	ttc	aga	att	gga	ttt		1
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1

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Leu Met Asn Glu Met Arg Arg Ile Thr Ser Asp Phe Arg Ile Gly Phe 50 55 60

Gly Ser Phe Val Glu Lys Thr Val Met Pro Tyr Ile Ser Thr Thr Pro 65 70 75 80

Ala Lys Leu Arg Asn Pro Cys Thr Ser Glu Gln Asn Cys Thr Thr Pro 85 90 95

Phe Ser Tyr Lys Asn Val Leu Ser Leu Thr Asn Lys Gly Glu Val Phe

Asn Glu Leu Val Gly Lys Gln Arg Ile Ser Gly Asn Leu Asp Ser Pro 115 120 125

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Gly Phe	e His	Phe	Ala 165	Gly	Asp	Gly	Lys	Leu 170	Gly	Gly	Ile	Val	Leu 175	Pro
Asn Ası	o Gly	Glņ 180	Cys	Ḥis	Leu	Glu	Asn 185	Asn	Met	Tyr	Thr	Met 190	Ser	His
Tyr Ty	r Asp 195	Tyr	Pro	Ser	Ile	Ala 200	His	Leu	Val	Gln	Lys 205	Leu	Ser	Glu
Asn Ası 21		Gln	Thr	Ile	Phe 215	Ala	Val	Thr	Glu	Glu 220	Phe	Gln	Pro	Val
Tyr Lys 225	s Glu	Leu	Lys	Asn 230	Leu	Ile	Pro	Lys	Ser 235	Ala				
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96 96	caa	gca	gcc	gcg	ttc	aac	gta	acg	ttt	cgt	cgc	gca	aaa	gga	tac		
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His	Val	Leu	Lys	Leu	Thr	Asn	Asņ	Ser	Asn	Gln	Phe	Gln	Thr	Glu	Val		
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Asn	Val	Thr	Arg	Leu	Leu	Val	Phe	Ala	Thr	Asp	Asp	Gly	Phe	His	Phe		
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gct 76	gġa	gat	gg¢	aag	cta	999	gcg	att	ctt	acc	cct	aac	gac	aaa	cga		5
	Gly	Asp	Gly	Lys	Leu	Gly	Ala	Ile	Leu	Thr	Pro	Asn	Asp	Gly	Arg		
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180 185 190 tqt cac ctc qaa qac aac cta tat aag aga agt aat gaa ttc gat tat Cys His Leu Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp Tyr 200 205 195 cca tct gtg gga caa ctg gcg cat aag ttg gct gag aac aac ata cag 6 Pro Ser Val Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile Gln 220 215 210 cca atc tit gca gtt aca agt cga atg gtg aaa aca tac gaa aaa ctt Pro Ile Phe Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys Leu 230 235 240 225 7 acg gaa atc atc cct aaa agt gcg Thr Glu Ile Ile Pro Lys Ser Ala 245 109 <210> <211> 248 <212> PRT <213> Artificial Sequence <220> Description of Artificial Sequence: Integrin <223> <400> 109 Gly Gln Lys Gln Leu Ser Pro Gln Lys Val Thr Leu Tyr Leu Arg Pro 15 10 Gly Gln Ala Ala Ala Phe Asn Val Thr Phe Arg Arg Ala Lys Gly Tyr

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Asn 65	Glu	Ile	Thr	Glu	Ser 70	Gly	Arg	Ile	Gly	Phe 75	Gly	Ser	Phe	Val	Asp 80
Lys	Thr	Val	Leu	Pro 85	Phe	Val	Asn	Thŗ	His 90	Pro	Asp	Lys	Leu	Arg 95	Asn
Pro	Cys	Pro	Asn 100	Lys	Glu	Lys	Glu	Cys 105	Gln	Pro	Pro	Phe	Ala 110	Phe	Arg
His	Val	Leu 115	Lys	Leu	Thr	Asn	Asn 120	Ser	Asn	Gln	Phe	Gln 125	Thr	Glu	Val
Gly	Lys 130	Gln	Leu	Ile	Ser	Gly 135	Asn	Leu	Asp	Ala	Pro 140	Glu	Gly	Gly	Leu
Asp 145	Ala	Met	Met	Gln	Val 150	Ala	Ala	Cys	Pro	Glu 155	Glu	Ile	Gly	Trp	Arg 160
Asn	Val	Thr	Arg	Leu 165	Leu	Val	Phe	Ala	Thr 170	Asp	Asp	Gly	Phe	His 175	Phe
Ala	Gly	Asp	Gly 180	Lys	Leu	Gly	Ala	Ile 185	Leu	Thr	Pro	Asn	Asp 190	Gly	Arg
Cys	His	Leu 195	Glu	Asp	Asn	Leu	Tyr 200	Lys	Arg	Ser		Glu 205	Phe	Asp	Tyr
Pro	Ser	Val	Gly	Gln	Leu	Ala	His	Lys · Page		Ala	Glu	Asn	Asn	Ile	Gln

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Pro Ile 225	Phe	Ala	Val	Thr 230	Ser	Arg	Met	Val	Lys 235	Thr	Tyr	Glu	Lys	Leu 240		
Thr Glu	Ile	Ile	Pro 245	Lys	Ser	Ala	٠									
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Tyr Pro	Ile	Asp	Leu	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Tyr	Ser	Met	Leu		
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gac gat 96	cta	cgt	aac	gtt	aag	aaa	ctt	gga	ggt	gat	tta	cta	aga	gct		
Asp Asp	Leu	Arg	Asn	Val	Lys	Lys	Leu	Gly	Gly	Asp	Leu	Ĺeu	Arg	Ala	•	
		20					25	•				30				
									•	_						
ctt aac 44	gaa	atc	aċg	gag	agt	aaa	cga	atc	ggc	ttc	ggc	tċa	ttc	gtc	•	1
Leu Așn	Glu	Ile	Thr	Glu	Ser	Gly	Arg	Ile	Gly	Phe	Gly	Ser	Phe	Val	•	
	35				,	40				•	45					
gac aag 92	aca	gta	ttg	ccc	ttc	gta ·	aac	acg	cac	cca	gac	aag	ctt	aga		1

# 130588.00025.ST25.txt Asp Lys Thr Val Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg . 60 55 50 aac ccc tgc cca aat aaa gag aaa gag tgt caa ccc ccg ttt gcc ttt 40 Asn Pro Cys Pro Asn Lys Glu Lys Glu Cys Gln Pro Pro Phe Ala Phe 80 70 75 65 aga cat gtc tta aag ctc acg aat aac agc aat cag ttt cag aca gaa 2 Arg His Val Leu Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu 90 95 85 gtt gga aaa caa ctg ata tcg ggt aat cta gac gca cca gag ggg gga 3 Val Gly Lys Gln Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly 110 100 105 3 ett gat gee atg atg eag gtg gea gee tge eeg gag gaa att ggg tgg Leu Asp Ala Met Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp 125 120 115 . agg aat gtc aca aga ctg cta gtt ttc gca act gat gac ggg ttt cat Arg Asn Val Thr Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His 135 140 130 ttt qct qqa qat qqt aaa ctq qqc gca att ttg act cct aac gat gga Phe Ala Gly Asp Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly 160 150 155 145 cgg tgt cat ttg gaa gac aac ctc tat aaa aga agc aat gaa ttc gac 5

						T30	588.	0002	5.51	25.c	XC .						
28 Arg	Cys	His	Leu	Glu	Asp	Asn	Leu	Tyr	Lys	Arg	Ser	Asņ	Glu	Phe	Asp		
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	cct	agt	gta	ggt	caa	tta	gcg	cac	aag	tta	gca	gaa	aac	aat	ata	•	5
76 Tyr	Pro	Ser	Val	Gly	Gln	Leu	Ala	His	Lys	Leu	Ala	Glu	Asn	Asn	Ile		
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	•		100				·										
caa	ccg	ata	ttt	gcg	gtt	acc	agt	cgc	atg	gtg	aaa	aca	tac	gaa	aag		6
24 Gln	Pro	Ile	Phe	Ala	Val	Thr	Ser	Arg	Met	Val	Lys	Thr	Tyr	Glu	Lys		
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tta	acc	qaq	ata	att	cca	aaa	tct	gct	gtg	ggc	gag	ctc	tcc	gaa	gat		6
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Leu	ınr	GIU	ire	iie	Pro	гуя	ser	Ala	vai	GIY		ьeu	ser	GIU	Asp		
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Ser	Ser	Asn	Val	Val	His	Leu	Ile	Lys	Asn	Ala	Tyr	Asn	Lys	Leu	Ser		
225					230					235				,	240		
agt 68	aga	gta	ttt	ttg	gac	cat	aat	gcg	cţţ	cct	gaţ	act	ctc	aag	gtg		7
	Arg	Val	Phe	Leu	Asp	Hiş	Asn	Ala	Leu	Pro	Asp	Thr	Leu	Lys	Val		
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- Leu Asn Glu Ile Thr Glu Ser Gly Arg Ile Gly Phe Gly Ser Phe Val 35 40 45
- Asp Lys Thr Val Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg
  50 55 60
- Asn Pro Cys Pro Asn Lys Glu Lys Glu Cys Gln Pro Pro Phe Ala Phe 65 70 75 80
- Arg His Val Leu Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu 85 90 95
- Val Gly Lys Gln Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly
  100 105 110
- Leu Asp Ala Met Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp
  115 120 125
- Arg Asn Val Thr Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His 130 135 140
- Phe Ala Gly Asp Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly Page 84

Arq Cys His Leu Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp 170

Tyr Pro Ser Val Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile 185 180

Gln Pro Ile Phe Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys 200 205 195

Leu Thr Glu Ile Ile Pro Lys Ser Ala Val Gly Glu Leu Ser Glu Asp 220 215 210

Ser Ser Asn Val Val His Leu Ile Lys Asn Ala Tyr Asn Lys Leu Ser 230 235 225

Ser Arg Val Phe Leu Asp His Asn Ala Leu Pro Asp Thr Leu Lys Val 250 . 245

Thr Tyr Asp Ser Phe 260

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Arg Asn Val Lys Lys

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Glu Leu Ser Glu Asp Ser Ser Asn Val Val His Leu Ile Lys Asn Ala
                               Page 88
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1			•	5	•				10					15			
	aac	aaa	cta	agt	tcg	aga	gtt	ttc	tta	gac	cac	aat	gca	ctg	cca		
96 Tyr	Asn	Lys	Leu	Ser	Ser	Arg	Val	Phe	Leu	Asp	His	Asn	Ala	Leu	Pro	•	
			20					25					30				
							,										-
gat 44	acg	ttg	aag	gta	aca	tac	gac	agc	ttt	tgc	tcc	aat	aaa	gtg	acc		. 1
Asp	Thr	Leu	Lys	Val	Thr	Tyr	Asp	Ser	Phe	Cys	Ser	Asn	Gly	Val	Thr		
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			•														
cat 92`	aga	aac	cag	cca	aga	ggc	gat	tgt	gac	gga	gta	caa	ata	aat	gta		1
His	Arg	Asn	Gln	Pr.o	Arg	Gly	Asp	Cys	Asp	Gly	Val	Gln	Ile	Asn	Val		
	50					55			-		60						
•	•																
cca 40	ata	aca	ttc	cag	gtt	aag	gtg	aca	gct	act	gag	tgt	ata	caa	gaa		2.
Pro	Ile	Thr	Phe	Gln	Val	Lys	Val	Thr	Ala	Thr	Glu	Cys	Ile	Gln	Glu		
65					70					75					80		
caa 67	agt	ttt	gta	att	aga	gcg	ctt	ggt									2
Gln	Ser	Phe	Val	Ile	Arg	Ala	Leu	Gly	•								
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Page 89

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Tyr Asn Lys Leu Ser Ser Arg Val Phe Leu Asp His Asn Ala Leu Pro 20 25 30

Asp Thr Leu Lys Val Thr Tyr Asp Ser Phe Cys Ser Asn Gly Val Thr 35 40 45

His Arg Asn Gln Pro Arg Gly Asp Cys Asp Gly Val Gln Ile Asn Val 50 55 60

Pro Ile Thr Phe Gln Val Lys Val Thr Ala Thr Glu Cys Ile Gln Glu 65 70 75 80

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Gly Phe Thr Asp Ile Val Thr Val Gln Val Leu Pro Gln Cys Glu Cys

1 5 10 , 15

aga tgt aga gat caa agt aga gac aga agt tta tgc cat gga aag ggc Page 90

130588.00025.ST25.txt Arg Cys Arg Asp Gln Ser Arg Asp Arg Ser Leu Cys His Gly Lys Gly 25 30 20 ttt tta gaa tgt gga atc tgt aga tgc gat acg gga tat ata gga aaa Phe Leu Glu Cys Gly Ile Cys Arg Cys Asp Thr Gly Tyr Ile Gly Lys 45 40 35 1 aat tgt gag tgt cag act caa ggg Asn Cys Glu Cys Gln Thr Gln Gly 55 50 123 <210> <211> 56 <212> PRT Artificial Sequence <213> <220> <223> Description of Artificial Sequence: Integrin <400> 123 Gly Phe Thr Asp Ile Val Thr Val Gln Val Leu Pro Gln Cys Glu Cys 10 Arg Cys Arg Asp Gln Ser Arg Asp Arg Ser Leu Cys His Gly Lys Gly 20 . 25

Phe Leu Glu Cys Gly Ile Cys Arg Cys Asp Thr Gly Tyr Ile Gly Lys

35 40 45

Asn Cys Glu Cys Gln Thr Gln Gly
50 55

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                                                           15
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                                10
                                                   15
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Ala Arg Lys Asn
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Ala Arg Lys Asn
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gga gac cta tta aga gca ttg aac gaa 75 Gly Asp Leu Leu Arg Ala Leu Asn Glu

20 25

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Asp Leu Ser Tyr Ser Leu Asp Asp Leu Arg Asn Val Lys Lys Leu Gly 1 5 10

Gly Asp Leu Leu Arg Ala Leu Asn Glu 20 25

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48 Asp	Tyr	Pro	Val	Asp	Ile	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Tyr	Ser	Met	
1				5					10					15		
aag 96	gac	gat	ctc	tgg	tca	att	cag	aac	ttg	gga	aca	aaa	cta	gca	aca	
	Asp	Asp	Leu	Trp	Ser	Ile	Gln	Asn	Ļeu	Gly	Thr	Lys	Leu	Ala	Thr	
			20					25					30			
caa 44	atg.	aga	aag	ctg	aca	tcg	aat	tta	aga	ata	gga	ttt	gga	gca	ttc	1
	Met	Arg	Lys	Leu	Thr	Ser	Asn	Leu	Arg	Ile	Gly	Phe	Gly	Ala	Phe	
		35					40					45				
	gat	aaa	cca	gta	agc	cct	tat	atg	tat	atc	tct	cca	ccg	gaa		1
89 Val	Asp	Lys	Pro	Val	Ser	Pro	Tyr	Met	Tyr	Ile	Ser	Pro	Pro	Glu		
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Asp 1	Tyr	Pro	Val	Asp 5	Ile	Tyr	Tyr	Leu	Met 10	Asp	Leu	Ser	Tyr	Ser 15	Met	
Lys	Asp	Asp	Leu 20	Trp	Ser	Ile	Gln	Asn 25	Leu	Gly	Thr	Lys	Leu 30	Ala	Thr	-
Gln	Met	Arg 35	Lys	Leu	Thr	Ser	Asn 40	Leu	Arg	Ile	Gly	Phe 45	Gly	Ala	Phe	
								Page	95			•				

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Val Asp Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu
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Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile
20 25 30

caa aat tta ggt acc aag ttg gcc acc caa atg cgt aaa tta act tca 44 Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met Arg Lys Leu Thr Ser 35

aat tta cgg ata gga ttc ggg gca ttt gtg gat aaa ccc gta tcg ccg 92 Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro 50

tac atg tat att agt cca cct gag gcg ctt gaa aac ccc tgc tac gac 2
40
Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp
65 70 75 80

atg aaa aca acg tgt ctg cct atg ttt ggc tac aag cat gtc cta aca 288
Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr

90 95

36	_	_	caa	_													3
Leu	Thr	Asp	Gln	Val	Thr	Arg	Phe	Asn	Glu	Glu	Val	Lys	Lys	Gln	Ser		
			100		•			105					110				
,						~~+	~~~	~~~						٠.			3
919 63	tet	cgc	aat	aga	gai	gcı	eeg	yaa								-	3
Val	Ser	Arg	Asn	Arg	Asp	Ala	Pro	Glu									
		115					120										
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Tyr	Leu	Met	Asp 20	Leu	Ser	Tyr	Ser	Met 25	Lys	Asp	Asp	Leu	Trp 30	Ser	Ile		
Gln	Asn	Leu 35	Gly	Thr	Lys	Leu	Ala 40	Thr	Gln	Met	Arg	Lys 45	Leu	Thr	Ser		•
Asn	Leu 50	Arg	Ile	Gly	Phe	Gly 55	Ala	Phe	Val	Asp	Lys 60	Pro	Väl	Ser	Pro		
Tyr 65	Met	Tyr	Ile	Ser	Pro 70	Pro	Glu	Ala	Leu	Glu 75	Asn	Pro	Cys	Tyr	Asp.		
Met	Lys	Thr	Thr	Cys	Leu	Pro	Met	Phe Page		Tyr	Lys	His	Val	Leu	Thr		

90 95

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Val Ser Arg Asn Arg Asp Ala Pro Glu 115 120

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10

15

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Trp Cys Ser Asp Glu Ala Leu Pro Leu Gly Ser Pro Arg

20 . 25

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                                 10
                                                    15
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Gln Val Thr Gln Val
           20
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Page 101

Ile Arg Ser

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Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr

20 25 30

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Thr Cys Leu Pro Met Phe Gly Tyr Lys

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Description of Artificial Sequence: Integrin

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Page 109

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Gln A	Ala	Gln	Ala	Glu	Pro	Asn	Ser	His	Arg	Cys	Asn	Asn	Gly	Asn	Gly		
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aca t 44	ttc	gaa	tgc	gga	gta	tgc	aga	tgc	gga	ccg	ggt	tgg	tta	999	agt	1	
Thr 1	Phe	Glu	Cys	Gly	Val	Cys	Arg	Cys	Gly	Pro	Gly	Trp	Leu	Gly	Ser		
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•																	
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Gln (	Cys	Glu	Cys	Ser	Glu	Glu	Asp	Tyr	Arg	Pro	Ser	Gln	Gln	Asp	Glu		
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Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr Cys Asn Arg

25 30 20

tat tgt aga gat gaa ata gag agc gtt aaa gag tta aaa gat aca ggt Page 113

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Asn Pro Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr 85 90 95

Lys His Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu
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1 5 10 15

atg aaa act acc tgc tta cca atg ttt gga tat aag cat gta tta aca 96 Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr

20 25 30

tta acg gac caa gta aca aga

17

Leu Thr Asp Gln Val Thr Arg

4 35

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Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr
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                                25
            20
Leu Thr Asp Gln Val Thr Arg
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130588.00025.ST25.txt
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Tyr Tyr Leu Met
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cca 96	gtc	gac	ata	tat	tac	ctc	atg	gac	ctg	agt	tac	agt	atg	aag	gat	
	Val	Asp	Ile	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Tyr	Ser	Met	Lys	Asp	
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gat 44	ctc	tgg	tca	att	caa	aat	cta	aaa	act	aag	ctt	gcg	acg	caa	atg	1
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	Lys	Leu	Thr	Ser	Asn	Leu	Arg	I·le	Gly	Phe	Gly	Ala	Phe	Val	Asp	
	50					55					60					
-	-					•										
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aac	ccc	tgc	tat	gac	atg	aaa		aca Page		tta	ccg	atg	ttt	ggt	tat	2

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88 Asn	Pro	Cys	Tyr	Asp	Met	Lys	Thr	Thr	Cys	Leu	Pro	Met	Phe	Gly	Tyr		
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aaa 36	cat	gtg	ctc	acg	ctt	acg	gac	caa	gtg	act	cgg	ttc	aat	gag	gaa		3
Lys	His	Val	Leu	Thr	Leu	Thr	Asp	Gln	Val	Thr	Arg	Phe	Asn	Glu	Glu		
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Val	Lys	Lys	Gln	Ser	Val	Ser	Arg	Asn	Arg	Asp	Ala	Pro	Glu	Gly	Gly		
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Arg	Asn	Asp	Ala	Ser	His	Leu	Leu	Val	Phe	Thr	Thr	Asp	Ala	Lys	Thr		
145					150					155					160		
cac 28	atc	gca	ttg	gat	ggt	aga	ttg	gct	gga	ata	gta	cag	cca	aat	gat		5
His	Ile	Ala	Leu	Asp	Gly	Arg	Leu	Ala	Gly	Ile	Val	Gln	Pro	Asn	Asp		
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	Gln	Cys	His	Val	Gly	Ser	Asp	Asn	His	Tyr	Ser	Ala	Ser	Thr	Thr		
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Asn	Leu	Asn	ьeu	iie	Pne		vaı	Thr	GIU	Asn		vai	Asn	ьeu	Tyr	
	210					215					220					
	aac	tac	tcg	gaa	ctg	ata	ccg	gga	aca	aca	gtt	999	gtc	ttg	tcc	7
20 Gln	Asn	Tyr	Ser	Glu	Leu	Ile	Pro	Gly	Thr	Thr	Val	Gly	Val	Leu	Ser	
225					230					235					240	
- 1				1-	- 1- 1-	1. I			- 1 1-				.			_
68	_	tca	-													7
Met	Asp	Ser	Ser	Asn	Val	Leu	Gln	Leu	Ile	Val	Asp	Ala	Tyr	Gly	Lys	
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16 Ile	Arg	Ser	Lys	Val	Glu	Leu	Glu	Val	Arg	Asp	Leu	Pro	Glu	Glu	Leu	
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Arg Asn Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr 145 150 155 160

His Ile Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp 165 170 175

Gly Gln Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr 190 185 180 Met Asp Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys 200 195 Asn Leu Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr 215 220 210 Gln Asn Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser 235 240 225 230 Met Asp Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys 245 Ile Arg Ser Lys Val Glu Leu Glu Val Arg Asp Leu Pro Glu Glu Leu 260 265 Ser Leu Ser Phe Asn Ala Thr 275 <210> 192 621 <211> <212> DNA <213> Artificial Sequence <220> Description of Artificial Sequence: Integrin <223> <220> <221> CDS <222> (1)..(621) <400> 192 gat gat tot aag aat ttt too ato cag gtt cga cag gtc gaa gat tac 48 Asp Asp Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr 10 15 1 5 Page 132

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Pro	Val	Asp	Ile	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Tyr	Ser	Met	Lys	Asp	
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gat 44	cta	tgg	agt	atc	caa	aac	ctg	ggc	acg	aaa	ctt	gcc	act	caa	atg	1
	Leu	Trp	Ser	Ile	Gln	Asn	Leu	Gly	Thr	Lys	Leu	Ala	Thr	Gln	Met	
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cgg 92	aaa	tta	aca	tca	aac	ttg	agg	att	ggc	ttt	999	gca	ttc	gtg	gat.	1
Arg	Lys	Leu	Thr	Ser	Asn	Leu	Arg	Ile	Gly	Phe	Gly	Ala	Phe	Val	Asp	
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aaa 40	ccc	gta	tcc	сса	tat	atg	tac	atc	tct	сса	ccg	gag	gca	ctc	gaa	2
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65					70					75					80	•
aac 88	cct	tgc	tac	gac	atg	aag	acc	aca	tgc	ctt	cct	atg	ttt	a aa	tat	2
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aaa 36	cac	gtg	ctt	act	tta	acc	gac	cag	gtt	acg	aga	ttc	aat	gaa	gag	. 3
Lys	His	Val	Leu	Thr	Leu	Thr	Asp	Gln	Val	Thr	Arg	Phe	Asn	Glu	Glu	
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gta 84	aaa	aag	caa	agt	gta	agc	cgt	aac	aga	gac	gca	ccg	gag	gga	3 93	3
	Lys	Lys	Gln	Ser	Val	Ser	Arg	Asn	Arg	Asp	Ala	Pro	Glu	Gly	Gly	

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	Asn	Asp	Ala	Ser	His	Leu	Leu	Val	Phe	Thr	Thr	Asp	Ala	Lys	Thr	
145					150					155					160	
										,						
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	Ile	Ala	Leu	Asp	Gly	Arg	Leu	Ala	Gly	Ile	Val	Gln	Pro	Asn	Asp	
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ggt 76	cag	tgt	cat	gtg	ggt	agt	gat	aat	cat	tat	agc	gct	tca	aca	acc	5
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atg 21	gac	tac	ćcc	agt	cta	gga	ctg	atg	acg	gaa	aag	ttg	tcg	caa		6
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<211 <212		207 PRT														
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<223> Description of Artificial Sequence: Integrin

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Asp	Leu	Trp 35	Ser	Ile	Gln	Asn	Leu 40	Gly	Thr	Lys	Leu	Ala 45	Thr	Gln	Met
Arg	Lys 50	Leu	Thr	Ser	Asn	Leu 55	Arg	Ile	Gly	Phe	Gly 60	Ala	Phe	Val	Asp
Lys 65	Pro	Val	Ser	Pro	Tyr 70	Met	Tyr	Ile	Ser	Pro 75	Pro	Glu	Ala	Leu	Glu 80
Asn	Pro	Cys	Tyr	Asp 85	Met	Lys	Thr	Thr	Cys 90	Leu	Pro	Met	Phe	Gly 95	Tyr
Lys	His		Leu ·100	Thr	Leu	Thr	Asp	Gln 105	Val	Thr	Arg	Phe	Asn 110	Glu	Glu
Val	Lys	Lys 115	Gln	Ser	Val	Ser	Arg 120	Asn	Arg	Asp	Ala	Pro 125	Glu	Gly	Gly
Phe	Asp 130	Ala	Ile	Met	Gln	Ala 135	Thr	Val	Cys	Asp	Glu 140	Lys	Ile	Gly	Trp
Arg 145	Asn	Asp	Ala	Ser	His 150	Leu	Leu	Val	Phe	Thr 155	Thr	Asp	Ala	Lys	Thr 160
His	Ile	Ala	Leu	Asp 165	Gly	Arg	Leu	Ala	Gly 170	Ile	Val	Gln	Pro	Asn 175	Asp
Gly	Gln	Cys	His 180	Val	Gly	Ser	Asp	Asn 185	His	Tyr	Ser	Ala	Ser 190	Thr	Thr

Met Asp Tyr Pro 195	Ser Leu Gly	Leu Met Th 200		eu Ser Gln 05	
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1	5	10	•	15	
gca cgg àgg gaa 96	gag ctc cta	gct agg gg	a tgc ccc c	tg gag gag	cta .
Ala Arg Arg Glu	Glu Leu Leu	Ala Arg Gl	y Cys Pro L	eu Glu Glu	Leu
20		25		30	
gaa gag cca cgt	gga cag caa	gag gta ct	a cag gat c	ag ccg ctg	tcg 1
44 Glu Glu Pro Arg	Gly Gln Gln	Glu Val Le	u Gln Asp G	ln Pro Leu	Ser
35	•	40	4	5	,
caa gga gcc cga	aat aaa aat	מכמ פכב כפ	g cta gca c	ra caa cgc	gta 1
92 Gln Gly Ala Arg			,		
50	_		60		
50	33				
cgc gtt aca tta	cgg cca ggc	gaa cca ca Page 13		ag gta aga	ttt 2

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ttg 88	cgt	gct	gaa	ggg	tat	ccg	gtg	gat	tta	tac	tat	ctc	atg	gat	ctt		2
	Arg	Ala	Glu	Gly	Tyr	Pro	Val	Asp	Leu	Tyr	Tyr	Leu	Met	Asp	Leu		
				85					90					95			
agt 36	tac	tcc	atg	aag	gat	gat	cta	gaa	agg	gta	cgc	caa	ctg	ggt	cat		3
	Tyr	Ser	Met	Lys	Asp	Asp	Leu	Glu	Arg	Val	Arg	Gln	Leu	Gly	His		
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gcc 84	tta	ttg	gta	aga	tta	caa	gaa	gta	aca	cat	agc	gta	cgt	atc	aaa		3
	Leu	Leu	Val	Arg	Leu	Gln	Glu	Val	Thr	His	Ser	Val	Arg	Ile	Gly		
	•	115					120					125					
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	130					135					140						
cct 80	agc	aaa	ttg	cgt	cac	cct	tgt	cca	act	agg	ctt	gag	cga	tgc	cag		4
	Ser	Lys	Leu	Arg	His	Pro	Cys	Pro	Thr	Arg	Leu	Glu	Arg	Cys	Gln		
145					150					155	-				160		
agt 28	ccg	ttc	tca	ttc	cac	cat	gtt	ttg	agt	tta	act	gga	gat	gcc	cag		5
-	Pro	Phe	Ser	Phe	His	His	Val	Leu	Ser	Leu	Thr	Gly	Asp	Ala	Gln		
				165					170					175			

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								•								
agt 24	CCC	gag	gga	999	ttt	gac	gcg	ata	ctt	caa	gca	gcg	ctc	tgt	cag	6
	Pro	Glu	Gly	Gly	Phe	Asp	Ala	Ile	Leu	Gln	Ala	Ala	Leu	Cys	Gln	
		195					200					205				
gaa 72	cag	att	ggc	tgg	cga	aac	gtc	agc	aga	cta	tta	gtc	ttt	acg	agt	6
Glu	Gln	Ile	Gly	Trp	Arg	Asn	Val	Ser	Arg	Leu	Leu	Val	Phe	Thr	Ser	
	210					215					220					
gac 20	gat	act	ttt	cac	aca	gca	aaa	gac	gga	aag	ctt	ggc	ggt	att	ttt	7
	Asp	Thr	Phe	His	Thr	Ala	Gly	Asp	Gly	Lys	Leu	Gly	Gly	Ile	Phe	
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atg 68	CCC	agc	gac	ggt	cat	tgt	cac	ctc	gat	tca	aat	gga	ttg	tac	agt	7
	Pro	Ser	Asp	Gly	His	Cys	His	Leu	Asp	Ser	Asn	Gly	Leu	Tyr	Ser	
				245					250					255		
cgg 16	tcc,	aca	gaa	ttc	gat	tat	cct	tcg	gtg	ggc	cag	gtg	gcg	cag	gca	8
	Ser	Thr	Glu	Phe	Asp.	Tyr	Pro	Ser	Val	Gly	Gln	Val	Ala	Gln	Ala	
			260					265					270			
ctg 64	agt	gct	gca	aac	atc	cag	cca	ata	ttt	gct	gtt	aca	tcg	gcg	gcg	8
	Ser	Ala	Ala	Asn	Ile	Gln	Pro	Ile	Phe	Ala	Val	Thr	Ser	Ala	Ala	
		275				,	280					285				

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ttg 12	ccg	gtt	tac	caa	gaa	ctc	tca	aaa	tta	ata	ccc	aaa	tcc	gct	gtc	9
	Pro	Val	Tyr	Gln	Glu	Leu	Ser	Lys	Leu	Ile	Pro	Lys	Ser	Ala	Val	
	290					295					300					
ggc 60	gaa	tta	tct	gag	gac	tcc	tca	aac	gtg	gtc	caa	ctc	atc	atg	gac	9
Gly	Glu	Leu	Ser	Glu	Asp	Ser	Ser	Asn	Val	Val	Gln	Leu	Ile	Met	Asp	
305					310					315					320	
gct 08	tat	aat	tcg	ctt	agt	agc	acg	gta	aca	ctg	gaa	cac	tca	tcg	ctt	10
Ala	Tyr	Asn	Ser	Leu	Ser	Ser	Thr	Val	Thr	Leu	Glu	His	Ser	Ser	Leu	
				325					330					335		
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Description of Artificial Sequence: Integrin <223>

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130588.00025.ST25.txt Glu Glu Pro Arg Gly Gln Glu Val Leu Gln Asp Gln Pro Leu Ser

Gln	Gly	Ala	Arg	Gly	Glu	Gly	Ala	Thr	Gln	Leu	Ala	Pro	Gln	Arg	Val
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Arg	Val	Thr	Leu	Arg	Pro	Gly	Glu	Pro	Gln	Gln	Leu	Gln	Val	Arg	Phe
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Phe	Gly	Ser	Phe	Val	Asp	Lys	Thr	Val	Leu	Pro	Phe	Val	Ser	Thr	Val
	130					135					140				

Pro	Ser	Lys	Leu	Arg	His	Pro	Cys	Pro	Thr	Arg	Leu	Glu	Arg	Cys	Gln
145					150					155					160

Ser	Pro	Phe	Ser	Phe	His	His	Val	Leu	Ser	Leu	Thr	Gly	Asp	Ala	Gln
				165					170					175	

Ala Phe Glu Arg Glu Val Gly Arg Gln Ser Val Ser Gly Asn Leu Asp

Ser Pro Glu Gly Gly Phe Asp Ala Ile Leu Gln Ala Ala Leu Cys Gln

Glu Gln Ile Gly Trp Arg Asn Val Ser Arg Leu Leu Val Phe Thr Ser

130588.00025.ST25.txt Asp Asp Thr Phe His Thr Ala Gly Asp Gly Lys Leu Gly Gly Ile Phe 235 230 225 Met Pro Ser Asp Gly His Cys His Leu Asp Ser Asn Gly Leu Tyr Ser 245 250 Arg Ser Thr Glu Phe Asp Tyr Pro Ser Val Gly Gln Val Ala Gln Ala 270 260 265 Leu Ser Ala Ala Asn Ile Gln Pro Ile Phe Ala Val Thr Ser Ala Ala 280 275 Leu Pro Val Tyr Gln Glu Leu Ser Lys Leu Ile Pro Lys Ser Ala Val 300 290 295 Gly Glu Leu Ser Glu Asp Ser Ser Asn Val Val Gln Leu Ile Met Asp 310 315 320 305 Ala Tyr Asn Ser Leu Ser Ser Thr Val Thr Leu Glu His Ser Ser Leu 325 330 Pro Pro Gly Val His Ile Ser Tyr Glu Ser Gln Cys Glu Gly Pro 340 345 <210> 196 273 <211> <212> DNA <213> Artificial Sequence <220> Description of Artificial Sequence: Integrin <223> <220> <221> CDS (1)..(273) <222> <400> 196 agt ttt gtt gat aaa aca gtc ctg ccg ttc gta agt acc gta cca agt 48

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	Pne	vai	Asp	_	1111	vai	ьец	PIO	10	vai	261	1111	vai	15	Ser	
1				5					10					10		
_	tta	cgc	cat	cca	tgt	cca	acg	agg	ttg	gag	aga	tgc	cag	tct	cct	
96 Lys	Leu	Arg	His	Pro	Cys	Pro	Thr	Arg	Leu	Gļu	Arg	Cys	Gln	Ser	Pro	
		,	20					25					30			
		+ +	~~~	~~+		++-	200	at a	a a t	aat	G 2 G	aat	C 2 2	acc	+++	1
44								cta								1
Phe	Ser		HIS	HIS	vai	Leu		Leu	Thr	GIÀ	Asp		GIII	Ата	Pne	
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											<i>c</i> 0					
	50					55					60					
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40	gga					ata					ctc					2
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<223> Description of Artificial Sequence: Integrin

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gcc 96	agg	cga	gaa	gaa	tta	ttg	gca	cgc	999	tgt	ccc	ctg	gag	gag	ctt		
	Arg	Arg	Glu	Glu	Leu	Leu	Ala	Arg	Gly	Cys	Pro	Leu	Glu	Glu	Leu		
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	~~~	cca	~~~	aat	<b>G</b> 2 <b>G</b>	aza	~ ~ ~	at t	tta	Caa	cat	caa	CCA	tta	agt		1
44																	_
Glu	Glu	Pro	Arg	Gly	Gln	Gln	Glu	Val	Leu	GIn	Asp	GIn	Pro	Leu	Ser		
		35					40					45					
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65					70					75					80		
													_			•	
ctt 88	cgg	gcc	gag	ggt	tac	ccg	gta	gat	ctg	tac	tac	cta	atg	gac	ctc		2
	Arg	Ala	Glu	Gly	Tyr	Pro	Val	Asp	Leu	Tyr	Tyr	Leu	Met	Asp	Leu		
				85			•		90					95			
							,										
agt 12	tat	agt	atg	aag	gac	gat	cta								•		3
Ser	Tyr	Ser	Met	Lys	Asp	Asp	Leu										
			100										*				
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<213> Artificial Sequence

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	Ile	Asn	Gln	Thr	Val	Thr	Phe	Trp	Val	Ser	Leu	Gln	Ala	Thr	His	
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	tta	ccc	gaa	cca	cat	ttg	cta	cgc	ctc	cgg	gct	tta	999	ttt	tct	1
44 Cys	Leu	Pro	Glu	Pro	His	Leu	Leu	Arg	Leu	Arg	Ala	Leu	Gly	Phe	Ser	
		35					40					45				
gag 92	gag	ctc	ata	gtt	gag	cta	cac	acg	tta	tgt	gac	tgc	aat	tgc	tca	1
	Glu	Leu	Ile	Val	Glu	Leu	His	Thr	Leu	Cys	Asp	Cys	Asn	Cys	Ser	
	50					55					60			-		
-	acg	caa	сса	caa	gcg	cca	cac	tgt	tcc	gat	999	cag	999	cac	ctt	2
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	tgt	gga	gtc	tgt	agt	tgc	gct	cct	ggt	aga	ttg	ggt	agg	ctg	tgc	2
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				85					90					95		
gag 36	tgc	agt	gta	gct	gag	tta	tcg	agt	cct	gat	ctc	gaa	agc	gga	tgt	3
	Cys	Ser	Val	Ala	Glu	Leu	Ser	Ser	Pro	Asp	Leu	Glu	Ser	Gly	Cys	
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cgc 84	gcg	ccg	aat	999	act	gga	cct	ctg	tgt	tcc	gga	aaa	999	cat	tgc	3
Arg	Ala	Pro	Asn	Gly	Thr	Gly	Pro	Leu	Cys	Ser	Gly	Lys	Gly	His	Cys	
		115					120					125				
								-								
cag 32	tgt	ggt	cgg	tgc	tct	tgc	tcg	ggt	cag	tca	agt	ggc	cat	ttg	tgc	4
	Cys	Gly	Arg	Cys	Ser	Cys	Ser	Gly	Gln	Ser	Ser	Gly	His	Leu	Cys	
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	tgt	gac	gac	gcc	agc	tgt	gaa	cgg	cat	gag	ggc	att	ttg	tgc	<b>3</b> 99	4
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ggt 28	ttc	ggc	agg	tgc	cag	tgt	999	gtg	tgt	cac	tgt	cat	gca	aac	cga	5
	Phe	Gly	Arg	Cys	Gln	Cys	Gly	Val	Cys	His	Cys	His	Ala	Asn	Arg	
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Thr	Gly	Arg	Ala	Cys	Glu	Cys	Ser	Gly	Asp	Met	Asp	Ser	Cys	Ile	Ser	
			180					185					190			•
ccg 24	gag	gga	ggt	tta	tgc	agt	ggt	cat	gga	aga	tgc	aag	tgc	aat	cgc	6
Pro	Glu	Gly	Gly	Leu	Cys	Ser	Gly	His	Gly	Arg	Cys	Lys	Cys	Asn	Arg	
		195					200					205				
, 							<b>.</b>					<del>-</del> -		L	·	_
72															cca ·	6
Cys	Gln	Cys	Leu	Asp	Gly	Tyr	Tyr	Gly	Ala	Leu	Cys	Asp	Gln	Cys	Pro	
	210					215					220					

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	tgt	aag	act	cca	tgt	gaa	aga	cac	cga	gac	tgc	gca	gag	tgc	ggt	7
20 Gly	Cys	Lys	Thr	Pro	Cys	Glu	Arg	His	Arg	Asp	Cys	Ala	Glu	Cys	Gly	
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gcg 68	ttt	aga	aca	ggc	ccc	ctg	gcc	acc	aat	tgc	agc	aca	gct	tgt	gct	7
	Phe	Arg	Thr	Gly	Pro	Leu	Ala	Thr	Asn	Cys	Ser	Thr	Ala	Cys	Ala	,
				245					250					255		
	act	aat	ġtġ	acg	ctt	gca	ctt	gcg	ccc	ata	tta	gat	gac	ggc	tgg	8
16 His	Thr	Asn	Val	Thr	Leu	Ala	Leu	Ala	Pro	Ile	Leu	Asp	Asp	Gly	Trp	
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	Lys	Glu	Arg	Thr	Leu	Asp	Asn	Gln	Leu	Phe	Phe	Phe	Leu	Val	Glu	
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	gat		aga	ggc	acg	gta		ctc	cgt	gtt	aga ⁻		caa	gaa	aag	9
12		gcc					gtt	ctc Leu				ccg				9
12		gcc					gtt					ccg				9
12 Asp gga	Asp 290	gcc Ala	Arg	Gly	Thr	Val 295	gtt Val		Arg	Val	Arg	ccg Pro	Gln	Glu	Lys	9
12 Asp gga 60	Asp 290 gca	gcc Ala	Arg	Gly	Thr	Val 295 gca	gtt Val	Leu	Arg ctg	Val 999	Arg 300 tgt	ccg Pro	Gln ggg	Glu gga	Lys atc	
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12 Asp gga 60 Gly 305 gtc 08	Asp 290 gca Ala	gcc Ala gat Asp	Arg cat His	Gly acc Thr	Thr caa Gln 310	Val 295 gca Ala	gtt Val att Ile gta	Leu gta Val	Arg ctg Leu	yal ggg Gly 315 tat	Arg 300 tgt Cys	ccg Pro gtt Val	ggg Gly tca	Glu gga Gly gtc	atc Ile 320	9
12 Asp gga 60 Gly 305 gtc 08	Asp 290 gca Ala	gcc Ala gat Asp	Arg cat His	Gly acc Thr	Thr caa Gln 310	Val 295 gca Ala	gtt Val att Ile gta Val	Leu gta Val	ctg Leu gcg Ala	yal ggg Gly 315 tat	Arg 300 tgt Cys	ccg Pro gtt Val	ggg Gly tca	Glu gga Gly gtc	atc Ile 320	9

atc tat gat

17

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Arg	Ala	Pro	Asn	Gly	Thr	Gly	Pro	Leu	Cys	Ser	Gly	Lys	Gly	His	Cys
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Gln	Cys	Gly	Arg	Cys	Ser	Cys	Ser Gly	Gln	Ser	Ser	Gly	His	Leu	Cys
	130					135				140				

Cys Gln Cys Leu Asp Gly Tyr Tyr Gly Ala Leu Cys Asp Gln Cys Pro 210 215 220

Gly	Cys	Lys	Thr	Pro	Cys	Glu	Arg	His	Arg	Asp	Cys	Ala	Glu	Cys	Gly
225					230		•			235					240

Ala	Phe	Arg	Thr	Gly	Pro	Leu	Ala	Thr	Asn	Cys	Ser	Thr	Ala	Cys	Ala
				245					250					255	

Cys Lys Glu Arg Thr Leu Asp Asn Gln Leu Phe Phe Leu Val Glu 275 280 285

Asp Asp Ala Arg Gly Thr Val Val Leu Arg Val Arg Pro Gln Glu Lys 290 295 300

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Description of Artificial Sequence: Integrin

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Glu His Ile Pro Ala

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                                      10
                                                           15
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Val Thr Ser Ala
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Val Thr Ser Ala
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